

FIGURE 1
Schematic representation of a typical immunoglobulin

tthl11 tthl11 hphi has
GTTGCTGTGG TTGTCTGGTG TTGAAGGAGA CATTGTGATG ACCCAGTCTC ACAAATTCAT GTCCACATCA GTAGGAGACA GGGTCAGCAT CACCTGCAAG
CAACGACCC AACAGACCAC AACTTCCTCT GTAACACTAC TGGGTCAGAG TGTTTAAGTA CAGGTGTAGT CATCCTCTGT CCCAGTCGTA GTGGACGTTC haeI sfaNI fnu4HI scrf1 ncil fokl bbv ecoRii ecoRii hpali hint GCCAGTCAGG ATGTGGGTGC TGCTATAGCC TGGTATCAAC AGAAACCAGG ACAATCTCCT AAACTACTGA TTTACTGGGC ATCCACCCGG CACACTGGAG CGGTCAGTCC TACACCCACG ACGATATCGG ACCATAGTTG TCTTTGGTCC TGTTAGAGGA TTTGATGACT AAATGACCCG TAGGTGGGCC GTGTGACCTC 101 sfaNI xhol I sau3A s au 3A dpn1 dpn1 hphI
TCCCTGATCS CTTCACAGGC AGTGGATCTG GGACAGATTT CACTCTCACC ATTAGCAATG TGCAGTCTGA TGACTTGGCA GATTATTCT GTCAACAATA
AGGGACTAGC GAAGTGTCCG TCACCTAGAC CCTGTCTAAA GTGAGAGTGG TAATCGTTAC ACGTCAGACT ACTGAACCGT CTAATAAAGA CAGTTGTTAT 201 sau96 mnli avali alui alui sfani bby mboli
TAGCGGGTAT CCTCTCACGT TCGGTGCTGG GACCAAGCTG GAGCTGAAAC GGGCTGATGC TGCACCAACT GTATCCATCT TCCCACCATC CAGTGAGCAG
ATCGCCCATA GGAGAGTGCA AGCCACGACC CTGGTTCGAC CTCGACTTTG CCCGACTACG ACGTGGTTGA CATAGGTAGA AGGGTGGTAG GTCACTCGTC hincll 301 mnli
mnli ddei
xmmi
mtaacatctg Gaggtgccic agtcgtgtgc ticttgaaca actictaccc caaagacatc aatgccaagt ggaacattga tggcagtgaa cgacaaaatg
aattgtagac ctccacggag tcagcacacg aagaacttgt tgaagatggg gtitctgtag ttacagtica ccttctaact accgtcactt gctgttttac 401 SAUSA

dpn1

fnu4H1

hgaI bcli

GCGTCCTGAA CAGTTGGACT GATCAGGACA GCAAAGACAG CACCTACAGC ATGAGCAGCA CCCTCACGTT GACCAAGGAC GAGTATGAAC GACATAACAG

CGCAGGACTT GTCAACCTGA CTAGTCCTGT CGTTTCTGTC GTGGATGTCG TACTCGTCGT GGGAGTGCAA CTGGTTCCTG CTCATACTTG CTGTATTGTC 501 sau96 hgal haellI 601 alul alul mboll ddel mnll hgiA mil mnll AGCTCCCCAG CTCCATCCTA TCTTCCCTTC TAAGGTCTTG GAGGCTTCCC CACAAGCGAC CTACCACTGT TGCGGTGCTC CAAACCTCCT CCCCACCTCC TCCGAGGGTC GAGGTAGGAT AGAAGGGAAG ATTCCAGAAC CTCCGAAGGG GTGTTCGCTG GATGGTGACA ACGCCACGAG GTTTGGAGGA GGGGTGGAGG 701

nucleotides: 882

801

foki

mnlI

FIGURE

mnii mnii titotoctoct cotogoctitt atcaigctaa tattigcaga aaatattcaa taaagigagi cittigcacti ga Aagaggagga ggaggaaag gaaccgaaaa tagtacgatt ataaacgict ittataagit atticactca gaaacgigaa ci

Nucleotide sequence of pK17G4 cDNA insert, including Representative coding region.

		• •		•		•		•	
20 Ser AGC	50 trp UGG	ser UCU	asp GAU	140 tyr UAC	170 asp GAC	Ach l	AGACAAAGGUCCUGAGACGCCACCAGCUCCCAGCUCCAUCCUAUCUUCCCUUCUAA	ICCUACCACUGUUGCGGGUGCUCCAAACCUCCUCCCCCACCUCCUCUCUCCUCCCUUUCCUUGGCUUUUAUCAUGCUAAAAUUUGCAGAAAA	
val GUC	tyr UAC	gln	ala 600	phe UUC	lys AAA	lys AAG	ົດກວວ	GCAG	
arg AGG	ile AUU	asn, val AAU. GUG	arg CGG	asn AAC	ser AGC	his CAC	וכחתכ	AUUU	
a Sp GAC	Jeu CUG	asn. AAU	1ys AAA	asn AAC	asp GAC	thr	CUAL	UAAU	
91y 66A	leu CUA	ser AGC	Jeu CUG	leu UUG	gln CAG	ala GCC	. CAUC	AUG	
val GUA	1ys AAA	ile AUU	g lu GAG	phe UUC	asp GAU	cys glu UGU GAG	Vecuc	UAUC	
ser UCA	Procus	thr ACC	Jeu CUG	Cys UGC	thr ACU	cys UGU	/222	JONE S	
thr ACA	ser UCU	leu CUC	lys AAG	va] GUG	trp UGG	thr ACC	VGCUC	nnec	
ser UCC	gln	thr ACU	thr	val GUC	ser AGU	tyr UAU	CACC!	MCC	
met AUG	gly	phe UUC	91 <i>y</i> 666	ser UCA	asn AAC	ser AGC	CAC	מטטר	
phe UUC	40 CCA	70 asp GAU	100 ala 600	130 ala 6CC	160 1eu CUG	190 asn AAC	SACGO	נוככו	
1ys AAA	1ys AAA	thr	91y 66U	91y 660	va] GUC	his CAU.	cuGA(CCC	
his	gln CAG	91y 666	phe UUC	91 <i>y</i> 66A	9 ¹ y 660	arg CGA	Seuce	mon	
ser	gln	ser ucu	thr ACG	ser UCU	asn AAU	g lu GAA	CAAAC	ກວກເ	
gln CAG	tyr UAU	91y 66A	leu CUC	thr	gln CAA	tyr UAU	AGA(CCACC	
thr	trp UGG	ser AGU		leu UUA	arg CGA	g l u GAG	AM ON O	ວກເ	
val met GUG AUG	ala GCC	91y 660	tyr UAU	g In CAG	g l u GAA	a sp GAC	cys ugu	COC	
val GUG	ile AUA	thr	91y 666	g l u GAG	ser AGU	lys AAG	g Ju GAG	AAAC	
ile AUU	ala 6cu	phe UUC	ser AGC	s er AGU	91y 66C	thr	asn AAU	ງວດວະ	
asp GAC	ala GCU	arg CGC	tyr UAU	ser UCC	asp GAU	leu UUG	arg AGG	90993	
9 Jy 66A	30 91y 66U	60 asp GAU	90 CAA	120 pro CCA	150 11e AUU	180 thr ACG	210 asn AAC	3006	
glu GAA	va] 606	ord USS	cAA CAA	pro CCA	lys AAG	Jeu	phe UUC	SACU	
va]	asp	va] GUC	S. D.	phe UCC	trp UGG	thr		CUAC(JUGA
. gly	gln	, g1y 66A	phe UUC	ile AUC	lys AAG	s er AGC	lys AAG	GAC.	ACUU(
ser ucu	Ser	thr ACU	tyr UAU	ser UCC	val GUC	ser AGC	val GUC	CAAG) JUGC
Jen One	ala 600	his	asp GAU	val GUA	asn AAU	met ser AUG AGC	ile AUU	CCA	SUCUL
trp UGG	lys AAG	thr arg l ACC CGG (ala GCA	thr	ile AUC	s er AGC	ord CCC	CUUCC	GUGA
leu trp leu cug ugg uug	cys lys ala ser	thr	leu ala d UUG GCA G	pro	lys asp ile a	tyr ser i UAC AGC	thr ser pro ile val lys ACU UCA CCC AUU GUC AAG	SAGGI	UAAAI
Jeu UNG	thr	ser UCC	asp GAC	ala ala pro thr GCU GCA CCA ACU	1ys AAA	ser thr	thr	GGUCUUGGAGGCUUCCCCACAAGCGA	UAUUCAAUAAAGUGAGUCUUUGCACU
G	i le Auc	ala GCA	asp GAU	ala GCU	020	s er AGC	ser UCA	ທີ່ວ່ອ	UAU

FIGURE 3 Light (Kappa) chain amino acid sequence and codons

		hinfI		יין וואס		gge1	1-1-0-				
٠	1	GAGTCAGCA	C TGAACACGG	T GGGGAGTGC	1"ACTTGAAGO	G GCTCAGCTTG C CGAGTCGAAC	ATTTACCTTO TAAATGGAAC	ahe TCCTTGTTT1 AGGAACAAA	TESTESAÑ I	SF ANI CAGTGTGAAG GTCACACTEG	LEVICE D
ı				scrF	I sau96 mnll		fnu4HI	•			٠,
	101	hinfI GGAGTCTGGI CCTCAGACCI	hinfI G GGAGTCTTA C CCTCAGAATT	ecoR A TGGAGCCTG	II avall	G AAACTCTCCT C TTTGAGAGGA	firm vdd	TEGATTOACT	TTCAGTAGAT AAGTCATCTA	ATGCCATGTC TACGGTACAG	TTGGGTTCGC AACCCAAGCG
		hpal hinfl	II mnli mboli		`					hp	hI
!	201	CAGACTCCGG	G AGAAGAGGC1	T GGAGTGGGT A CCTCACCCA	C GCAACCATT G CGTTGGTAA	A GTAGTGGTGG T CATCACCACC	TAGTTCACAC ATCAAGTGTG fok1	CTTCCATCCA GAAGGTAGGT	GACAGTGTGA CTGTCACACT	AGGGCGATTC TCCCGCTAAG	ACCATCTCCA TGGTAGAGGT
						mnlI	mn 1 Í				
!	301	GAGACAATGO CTCTGTTACG	CAAGAACACC G GTTCTTGTGC	rsal C CTGTACCTG G GACATGGAC	C AAATGAGCA G TTTACTCGT	ddel dd G TCTGAGGTCT C AGACTCCAGA	GAGGACACGG	elll CCATGTATTA GGTACATAAT	CTGTGCAAGA GACACGTTCT	mnlI CCCCCTCTTA GGGGGAGAAT	TTTCGTTAGT AAAGCAATCA
								.*			xhoII
		-								sau	scrFI 96 sau3A
:					mnll dde	l hphI	mnlI ddel			hae	ecoRII.
	401	AGCGGACTAT TCGCCTGATA	GCTATGGACT CGATACCTGA	ACTGGGGTCA A TGACCCCAG Scri	A AGGAACCTC	A GTCACCGTCT T CAGTGGCAGA	CCTCAGCCAA	AACGACACCC TTGCTGTGGG	CCATCTGTCT GGTAGACAGA	ATCCACTGGC TAGGTGACCG	CCCTCCATCT
!			ncol	i sfaNI	foki					xholl sau3A	
		fnu4HI bbv		hphI ecol	RII scrFi ecoRi		đđeľ		scrFI ecoRII	dpnI	
1	501	GCTGCCCAAA	CTAACTCCAT	GGTGACCCTG	GGATGCCTG	TCAAGGGCTA	TTTCCCTGAG	CCAGTGACAG	TGACCTGGAA	DamHI CTCTGGATCC	CTGTCCAGCG
į.		CGACGGGTTT	GATTGAGGTA	CCACTGGGA	CCTACGGAC	AGTTCCCGAT	AAAGGGACTC	GGTCACTGTC	ACTGGACCTT	GAGACCTAGG	GACAGGTCGC
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'		hg fA	. pvull alul	pstI	Ifom	ddel	v ddeI aluI	mn11	mn I I	el I I	ha h I
(601	GTGŤGCACAC	CTTCCCAGCT	GTCCTGCAGT	CTGACCTCTA	CACTCTGAGC	AGCTCAGTGA	CTGTCCCCTC	CAGCCCTCGG	CCCACCCACA	hphI CCGTCACCTG
		CALACGIGIG	GAAGGGILGA	LAGGALGICA	(GAL I GGAGA I	GTGAGACTCG	TCGAGTCACT	GACAGGGGAG	GTCGGGAGCC	GGGTCGCTCT	GGCAGTGGAC
			scrFI	•							
			haell ncil	fnu4HI			scrFI		,		
١,	701	DAACGTTGCC	I hpall	bbv GCAGCACCAA	GGTGGACAAG	AAAATTOTOO	oc of it	TCCTTCTAAC	ndeI	rsal	
'	, 01	GTTGCAACGG	GTGGGCCGGT	CGTCGTGGTT	CCACCTGTTC	AAAATTGTGC	GGTCCCTAAC	ACCAACATTC	GGAACGTATA	CATGTCAGGG	AGAAGTATCA TCTTCATAGT
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8				f	att bada		• • •			_	' .
, -	301	mboli TCTGTCTTCA	TCTTCCCCCC	AAAGCCCAAG	oki hgiA Gatetertra	CCATTACTCT	ddeI	CTCACCTCTC	acci	fo	ki avai
l	801	TCTGTCTTCA	TCTTCCCCCC	AAAGCCCAAG	GATGTGCTCA	CCATTACTCT GGTAATGAGA	CACTCCTAAC	GTCACGTGTG CAGTGCACAC	TTCTCCTACA	CATCACCA.	
	301	TCTGTCTTCA	TCTTCCCCCC	AAAGCCCAAG	GATGTGCTCA	CCATTACTCT GGTAATGAGA	GACTCCTAAG CTGAGGATTC	CAGTGCACAC	TTCTCCTACA	CATCACCA.	
	301	TCTGTCTTCA	TCTTCCCCCC	AAAGCCCAAG	GATGTGCTCA	CCATTACTCT GGTAATGAGA	CACTCCTAAC	CAGTGCACAC	TTCTCCTACA	CATCACCA.	
	301	TCTGTCTTCA	TCTTCCCCCC	AAAGCCCAAG	GATGTGCTCA	CCATTACTCT GGTAATGAGA	GACTCCTÁAG CTGAGGATTC smal scr scrF	CAGTGCACAC FI I	TTCTCCTACA	CATCACCA.	
		TCTGTCTTCA AGACAGAAGT	TCTTCCCCC AGAAGGGGGG	AAAGCCCAAG	GATGTGCTCA CTACACGAGT	CCATTACTCT GGTAATGAGA	GACTCCTÁAG CTGAGGATTC smal scr	CAGTGCACAC FI I I	TTCTCCTACA	CATCACCA.	
	301	TCTGTCTTCA AGACAGAAGT sau96 avalI	TCTTCCCCC AGAAGGGGGG PVuII aluI	AAAGCCCAAG	GATGTGCTCA CTACACGAGT mn1I	ddeI	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncil hpa	CAGTGCACAC	TTGTGGTAGA AACACCATCT	CATCAGCAAG GTAGTCGTTC	GATGATCCCG CTACTAGGGC
9	01	TCTGTCTTCA AGACAGAAGT Sau96 aval1 AGGTCCAGTT	TCTTCCCCCC AGAAGGGGGG PVuII aluI CAGCTGGTTT	AAAGCCCAAG TTTCGGGTTC	GATGTGCTCA CTACACGAGT mn11 hg1A TGGAGGTGCA	ddeI alul hg	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncil hpa aI avail	FI I I I II mnlI	TTGTGGTAGA	CATCAGCAAG GTAGTCGTTC	GATGATCCCG CTACTAGGGC
9		TCTGTCTTCA AGACAGAAGT Sau96 aval1 AGGTCCAGTT	TCTTCCCCCC AGAAGGGGGG PVuII aluI CAGCTGGTTT	AAAGCCCAAG TTTCGGGTTC	GATGTGCTCA CTACACGAGT mn11 hg1A TGGAGGTGCA	ddeI	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncil hpa aI avail	FI I I I II mnlI	TTGTGGTAGA	CATCAGCAAG GTAGTCGTTC	GATGATCCCG CTACTAGGGC
9		TCTGTCTTCA AGACAGAAGT Sau96 aval1 AGGTCCAGTT	PYUII alui CAGCTGGTTT GTCGACCAAA	AAAGCCCAAG TTTCGGGTTC	GATGTGCTCA CTACACGAGT mn11 hg1A TGGAGGTGCA	ddeI alul hg	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncil hpa aI avail	FI I I I GGGAGGAGCA CCCTCCTCGT	TTGTGGTAGA	CATCAGCAAG GTAGTCGTTC	GATGATCCCG CTACTAGGGC
	01	Sau96 aval1 AGGTCCAGTT TCCAGGTCAA	PVUII alui CAGCTGGTTT GTCGACCAAA	AAAGCCAAG TTTCGGGTTC TTTCGGGTTC GTAGATGATG GTAGATGATG CATCTACTAC	GATGTGCTCA CTACACGAGT Mn11 hg1A TGGAGGTGCA ACCTCCACGT	ddeI alui hg CACAGCTCAG GTGTCGAGTC	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncii hpa aI avai ACGCAACCCC TGCGTTGGGG	FI I I II mnll GGGAGGAGCA CCCTCCTCGT fnu4HI bby	TTGTGGTAGA AACACCATCT GTTCAACAGC CAAGTTGTCG	CATCAGCAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT
		Sau96 avaiI AGGTCCAGTT TCCAGGTCAA	PVUII alui CAGCIGGTTT GTCGACCAAA scrFI econii ATGCACCAGG	AAAGCCCAAG TTTCGGGTTC GTAGATGATG CATCTACTAC	MN11 hg 1A TGGAGGTGCA ACCTCCACGT	ddeI alul hg CACAGCTCAG GTGTCGAGTC	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncil hpa aI avai ACGCAACCCC TGCGTTGGGG	FI I I I I I GGGAGGAGCA CCCTCCTCGT fnu4HI bbv aluI	TTGTGGTAGA AACACCATCT GTTCAACAGC CAAGTTGTCG	CATCAGCAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT
	01	Sau96 avaiI AGGTCCAGTT TCCAGGTCAA	PVUII alui CAGCIGGTTT GTCGACCAAA scrFI econii ATGCACCAGG	AAAGCCCAAG TTTCGGGTTC GTAGATGATG CATCTACTAC	Mn11 hg 1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC	ddeI alui hg CACAGCTCAG GTGTCGAGTC	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncil hpa aI avai ACGCAACCCC TGCGTTGGGG	FI I I I I I GGGAGGAGCA CCCTCCTCGT fnu4HI bbv aluI	TTGTGGTAGA AACACCATCT GTTCAACAGC CAAGTTGTCG	CATCAGCAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT
	01	Sau96 avaiI AGGTCCAGTT TCCAGGTCAA	PVUII alui CAGCIGGTTT GTCGACCAAA scrFI econii ATGCACCAGG	AAAGCCCAAG TTTCGGGTTC GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT	Mn11 hg 1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC	ddeI alul hg CACAGCTCAG GTGTCGAGTC	GACTCCTAAG CTGAGGATTC smal scr scrf nci ncii hpa aI avai ACGCAACCCC TGCGTTGGGG hincii GGGTCAACAG CCCAGTTGTC	FI II mnli GGGAGGAGCA CCCTCCTCGT fnu4HI bby alui T6CAGCTTTC ACGTCGAAAG eIII	TTGTGGTAGA AACACCATCT GTTCAACAGC CAAGTTGTCG	CATCAGCAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT
1	01 .	Sau96 aval1 AGGTCCAGTT TCCAGGTCAA	PVUII alui CAGCTGGTTT GTCGACCAAA scrFI ecoRII ATGCACCAGG TACGTGGTCC	AAAGCCCAAG TTTCGGGTTC GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT	mn11 hg 1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC	ddeI alui hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncil hpa al aval ACGCAACCCC TGCGTTGGGG hincil GGGTCAACAG CCCAGTTGTC ha	FI I I II mnll GGGAGGAGCA CCCTCCTCGT fnu4HI bbv aluI T6CAGCTTTC ACGTCGAAAG elii	TTGTGGTAGA AACACCATCT GTTCAACAGC CAAGTTGTCG CCTGCCCCCA GGACGGGGGT	CATCAGCAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA taqI TCGAGAAAAC AGCTCTTTTG	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAA GTAGAGGTTT
1	01	Sau96 avail AGGTCCAGTT TCCAGGTCAA ACTTCCCATC TGAAGGGTAG	PYUII alui CAGCTGGTTT GTCGACCAAA scrFI ecoRII ATGCACCAGG TACGTGGTCC	GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT	mn11 hg 1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC	ddeI alul hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT	GACTCCTAAG CTGAGGATTC smal scr scrF nc i nc i1 hap aI aval ACGCAACCCC TGCGTTGGGG hincII GGTCAACAG CCCAGTTGTC ha hae	FI I I II mnli GGGAGGAGA CCCTCCTCGT fnu4HI bbv aluI TBCAGCTTTC ACGTCGAAAG	TTGTGGTAGA AACACCATCT GTTCAACAGC CCAAGTTGTCG CCTGCCCCCA GGACGGGGGT	CATCAGCAAG GTAGTCGTTC dde ACTITCCGCT TGAAAGGCGA taqI TCGAGAAAAC AGCTCTTTTG	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAA GTAGAGGTTT
1	01 .	Sau96 avail AGGTCCAGTT TCCAGGTCAA ACTTCCCATC TGAAGGGTAG	PYUII alui CAGCTGGTTT GTCGACCAAA scrFI ecoRII ATGCACCAGG TACGTGGTCC	GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT	mn11 hg 1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC	ddeI alui hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT mnli CACCTCCCAA	GACTCCTAAG CTGAGGATTC smal scr scrF nc i nc i1 hap aI aval ACGCAACCCC TGCGTTGGGG hincII GGTCAACAG CCCAGTTGTC ha hae	FI I I II mnli GGGAGGAGA CCCTCCTCGT fnu4HI bbv aluI TBCAGCTTTC ACGTCGAAAG	TTGTGGTAGA AACACCATCT GTTCAACAGC CCAAGTTGTCG CCTGCCCCCA GGACGGGGGT	CATCAGCAAG GTAGTCGTTC dde ACTITCCGCT TGAAAGGCGA taqI TCGAGAAAAC AGCTCTTTTG	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAA GTAGAGGTTT
1	01 .	sau96 aval1 AGGTCCAGTT TCCAGGTCAA ACTTCCCATC TGAAGGGTAG ACCAAAGGCA TGGTTTCCGT	PVUII aluI CAGCTGGTTT GTCGACCAAA scrFI ecoRII ATGCACCAGG TACGTGGTCC GGCCCGAAGGC CTGGCTTCCG	GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT TCCACAGGTG AGGTGTCCAC	mn11 hg1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC	ddeI alul hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT mn1I CACCTCCCAA GTGGAGGGTT fnu4HI	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncil hpa aI avai ACGCAACCCC TGCGTTGGGG hincil GGGTCAACAG CCCAGTTGTC ha hae bal GGAGCAGATG CCTCGTCTAC	FI II III mnli GGGAGGAGCA CCCTCCTCGT fnu4HI bbv aluI TBCAGCTTTC ACGTCGAAAG eIII II GCCAAGGATA CGGTTCCTAT	GTTCAACAGC CAAGTTGTCG CCTGCCCCCA GGACGGGGGT AAGTCAGTCT (TTCAGTCAGA (CATCAGCAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA taqI TCGAGAAAAC AGCTCTTTTG GAGCTCTTTTG GAGCACGTAC	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAA GTAGAGGTTT
1	01 .	Sau96 aval1 AGGTCCAGTT TCCAGGTCAA ACTTCCCATC TGAAGGGTAG ACCAAAAGGCA ACCAAAAGGCA TGGTTTCCGT mbol1 mbo	PVUII alui CAGCTGGTTT GTCGACCAAA SCFFI ecoRII ATGCACCAGG TACGTGGTCC GACCGAAGGC CTGGCTTCCG	GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT TCCACAGGTG AGGTGTCCAC	mn11 hg 1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC TACACCATTC ATGTGGTAAG	ddeI alul hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT mnll CACCTCCCAA GTGGAGGGTT fnu4HI bby	GACTCCTAAG CTGAGGATTC smal scr scrf nci ncii hpa aI avai ACGCAACCCC TGCGTTGGGG hincii GGGTCAACAG CCCAGTTGTC ha hae GGAGCAGCAGC	FI II III IIIIIIIIIIIIIIIIIIIIIIIIIIII	GTTCAACAGC CAAGTTGTCG CCTGCCCCCA GGACGGGGGT AAGTCAGTCT CCCCAACATCT CCCCCAACATCT CCCCAACATCT CCCCCAACATCT CCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCAACATCT CCCCCAACATCT CCCCAACATCT CCCCCAACATCT CCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCA	CATCAGCAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA taqI ICGAGAAAAC AGCTCTTTTG	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAA GTAGAGGTTT
1	001 .	Sau96 aval1 AGGTCCAGTT TCCAGGTCAA ACTTCCCATC TGAAGGGTAG ACCAAAAGGCA ACCAAAAGGCA TGGTTTCCGT mbol1 mbo	PVUII alui CAGCTGGTTT GTCGACCAAA SCFFI ecoRII ATGCACCAGG TACGTGGTCC GACCGAAGGC CTGGCTTCCG	GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT TCCACAGGTG AGGTGTCCAC	mn11 hg 1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC TACACCATTC ATGTGGTAAG	ddeI alul hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT mnll CACCTCCCAA GTGGAGGGTT fnu4HI	GACTCCTAAG CTGAGGATTC smal scr scrf nci ncii hpa aI avai ACGCAACCCC TGCGTTGGGG hincii GGGTCAACAG CCCAGTTGTC ha hae GGAGCAGCAGC	FI II III IIIIIIIIIIIIIIIIIIIIIIIIIIII	GTTCAACAGC CAAGTTGTCG CCTGCCCCCA GGACGGGGGT AAGTCAGTCT CCCCAACATCT CCCCCAACATCT CCCCAACATCT CCCCCAACATCT CCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCAACATCT CCCCCAACATCT CCCCAACATCT CCCCCAACATCT CCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCAACATCT CCCCCA	CATCAGCAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA taqI ICGAGAAAAC AGCTCTTTTG	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAA GTAGAGGTTT
1	001 .	Sau96 aval1 AGGTCCAGTT TCCAGGTCAA ACTTCCCATC TGAAGGGTAG ACCAAAAGGCA ACCAAAAGGCA TGGTTTCCGT mbol1 mbo	PVUII alui CAGCTGGTTT GTCGACCAAA SCFFI ecoRII ATGCACCAGG TACGTGGTCC GACCGAAGGC CTGGCTTCCG	GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT TCCACAGGTG AGGTGTCCAC	mn11 hg 1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC TACACCATTC ATGTGGTAAG	ddeI alul hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT mnll CACCTCCCAA GTGGAGGGTT fnu4HI bby	GACTCCTAAG CTGAGGATTC smal scr scrf nci ncii hpa aI avai ACGCAACCCC TGCGTTGGGG hincii GGGTCAACAG CCCAGTTGTC ha hae GGAGCAGCAGC	FI II III IIIIIIIIIIIIIIIIIIIIIIIIIIII	GTTCAACAGC CCAGCTCCCCCA AAGTCAGCCCCCA AAGTCAGCCC CTTCAGCCAGCCCCAC GCCCATCATG GCCCCATCATG Sau96	CATCAGCAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA taqI ICGAGAAAAC AGCTCTTTTG	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAA GTAGAGGTTT
1	001	sau96 aval1 AGGTCCAGTT TCCAGGTCAA ACTTCCCATC TGAAGGGTAG ACCAAAGGCA TGGTTTCCGT mbol1 mbo TCTTCCCTGA AGAAGGGACT acc1	PVUII aluI CAGCTGGTTT GTCGACCAAA scrFI ecoRII ATGCACCAGG TACGTGGTCC GGCCTCCG CTGGCTTCCG 11 AGACATTACT TCTGTAATGA	GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT TCCACAGGTG AGGTGTCCAC GTGGAGTGCCAC GTGGAGTGCCAC GTGGAGTGCCAC TDOLI	mn11 hg1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC TACACCATTC ATGTGGTAAG AGTGGAATGG TCACCTTACC	ddeI aluI hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT mnlI CACCTCCCAA GTGGAGGGTT fnuHI bbv GCAGCCAGCG CCTCGGTCGC	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncil hpa aI avai ACGCAACCCC TGCGTTGGGG hinclI GGGTCAACAG CCCAGTTGTC ha hae CCCAGTTGTC GGAGCAGATG CCTCGTCTAC GAGAACTACA CTCTTGATGT	FI I I II mnli GGGAGGAGCA CCCTCCTCGT fnu4HI bbv alul TSCAGCTTTC ACGTCGAAAG eIII I GCCAAGGATA CCGTCCTAT ddeI AGAACACTCA CTTGTGAGT	GTTCAACAGC CAAGTTGTCG CCTGCCCCCA AAGTCAGTCT AAGTCAGTCT TTCAGTCAGC CCGGTAGTAC Sau96 mn11	CATCAGCAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA taqI TCGAGAAAAC AGCTCTTTTG GTGGCTTTTG ACACGAATG ACACGAATG TTGTGCTTAC TGTGCTTAC	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAA GTAGAGGTTT ATAACAGACT IATTGTCTGA GCTCTTACTT CGAGAATGAA mbol
1	001 .	sau96 aval1 AGGTCCAGTT TCCAGGTCAA ACTTCCCATC TGAAGGGTAG ACCAAAAGGCA TGGTTTCCGT mbol1 mbo TCTTCCCTGA AGAAGGGACT acc1 CGTCTACAGC AGCACAGCA	PVUII alui CAGCTGGTTT GTCGACCAAA SCFFI ecoRII ATGCACCAGG TACGTGGTCC GACCGAAGGC CTGGCTTCCG	GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT TCCACAGGTG AGGTGTCCAC GTGGAGTGCCAC GTGGAGTGCCAC GTGGAGTGCCAC GTGGAGTGCCAC GTGGAGTGGC CACCTCACCG	mn11 hg 1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC TACACCATTC ATGTGGTAAG AGTGGAATGG TCACCTTACC	ddeI alul hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT mn11 CACCTCCCAA GTGGAGGGTT fnu4H1 bbv GCAGCCAGCG CCTCGGTCGC	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncii hpa aI avai ACGCAACCCC TGCGTTGGGG hincii GGGTCAACAG CCCAGTTGTC ha hae bal GGAGCAGCATG CCTCGTCTAC GAGAACTACA CTCTTGATGT	FI II III IIIIIIIIIIIIIIIIIIIIIIIIIIII	TTGTGGTAGA AACACCATCT GTTCAACAGC CAAGTTGTCG CCTGCCCCCA GGACGGGGGT AAGTCAGTCT CTTCAGTCAGA GCCCATCATG GCCCATCATG GCCGGTAGTAC sau96 mn11 haeIII	CATCAGGAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA taq1 TCGAGAAAAC GACCTCTTTTG GACCTCTTTTG AACACGAATG TTGGACGAACG TTGTGCTTAC	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAA GTAGAGGTTT ATAACAGACT IATTGTCTGA GCTCTTACTT GAGAAATGAA mbol ddeI
1	001	Sau96 aval1 AGGTCCAGTT TCCAGGTCAA ACTTCCCATC TGAAGGGTAG ACCAAAAGGCA TGGTTTCCGT mbol1 mbo TCTTCCCTGA AGAAGGGACT	PVUII alui CAGCTGGTTT GTCGACCAAA SCFFI ecoRII ATGCACCAGG TACGTGGTCC GACCGAAGGC CTGGCTTCCG	GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT TCCACAGGTG AGGTGTCCAC GTGGAGTGCCAC GTGGAGTGCCAC GTGGAGTGCCAC GTGGAGTGCCAC GTGGAGTGGC CACCTCACCG	mn11 hg 1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC TACACCATTC ATGTGGTAAG AGTGGAATGG TCACCTTACC	ddeI alul hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT mn11 CACCTCCCAA GTGGAGGGTT fnu4H1 bbv GCAGCCAGCG CCTCGGTCGC	GACTCCTAAG CTGAGGATTC smal scr scrF nci ncii hpa aI avai ACGCAACCCC TGCGTTGGGG hincii GGGTCAACAG CCCAGTTGTC ha hae bal GGAGCAGCATG CCTCGTCTAC GAGAACTACA CTCTTGATGT	FI II III IIIIIIIIIIIIIIIIIIIIIIIIIIII	TTGTGGTAGA AACACCATCT GTTCAACAGC CAAGTTGTCG CCTGCCCCCA GGACGGGGGT AAGTCAGTCT CTTCAGTCAGA GCCCATCATG GCCCATCATG GCCGGTAGTAC sau96 mn11 haeIII	CATCAGGAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA taq1 TCGAGAAAAC GACCTCTTTTG GACCTCTTTTG AACACGAATG TTGGACGAACG TTGTGCTTAC	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAA GTAGAGGTTT ATAACAGACT IATTGTCTGA GCTCTTACTT GAGAAATGAA mbol ddeI
1	001	sau96 aval1 AGGTCCAGTT TCCAGGTCAA ACTTCCCATC TGAAGGGTAG ACCAAAGGCA TGGTTTCCGT mbol1 mbo TCTTCCCTGA AGAAGGGACT accl CGTCTACAGC GCAGATGTCG	PVUII aluI CAGCTGGTTT GTCGACCAAA scrFI ecoRII ATGCACCAGG TACGTGGTCC GACCGAAGGC CTGGCTTCCG 11 AGACATTACT TCTGTAATGA aluI AAGCTCAATG TTCGGAGTTC scrI	GTAGATGATG GTAGATGATG CATCTACTAC ACTGGCTCAA TGACCGAGTT TCCACAGGTG AGGTGTCCAC GTGGAGTGCCAC GTGGAGTGCCAC GTGGAGTGCCAC GTGGAGTGCCAC GTGGAGTGCCAC TGCACAGGTGAGAGAGAGACGTCTTCTC FI sau	mn11 hg1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC AI TACACCATTC ATGTGGTAAG AGTGGAATGG TCACCTTACC mn11 CAACTGGGAG GTTGACCCTC 3A	ddeI alul hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT mn1I CACCTCCCAA. GTGGAGGGTT fbu4HI bbv GCAGCCAGCG CETCGGTCGC GCAGGAAATA GCGCCCTTTAT	GACTCCTAAG CTGAGGATTC smal scr scrF nci hpa aI avaI ACGCAACCCC TGCGTTGGGG hincII GGGTCAACAG CCCAGTTGTC ha hae bal GGAGCAGATG CCTCGTCTAC CTCTTGATGT hphl TTTTCACCTG GAAAGTGGAC Saug6	FI I I II mn 11 GGGAGGAGCA CCCTCCTCGT fnu4HI bbv alui TECAGCTTTC ACGTCGAAAG eIII I GCCAAGGATA CGGTTCCTAT ddeI AGAACACTCA CCTTGTGAGT CTCTGTGTTA	TTGTGGTAGA AACACCATCT GTTCAACAGC CAAGTTGTCG CCTGCCCCCA GGACGGGGGT AAGTCAGTCT CTTCAGTCAGA GCCCATCATG GCCCATCATG GCCGGTAGTAC sau96 mn11 haeIII	CATCAGGAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA taq1 TCGAGAAAAC GACCTCTTTTG GACCTCTTTTG AACACGAATG TTGGACGAACG TTGTGCTTAC	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAA GTAGAGGTTT ATAACAGACT IATTGTCTGA GCTCTTACTT GAGAAATGAA mbol ddeI
1 1:	001	sau96 aval1 AGGTCAGTT TCCAGGTCAA ACTTCCCATC TGAAGGGTAG ACCAAAGGCA TGGTTTCCGT mbol1 mbo TCTTCCCTGA AGAAGGGACT acc1 CGTCTACAGC GCAGATGTCG mn11 AAGAGCCTCT	PVUII aluI CAGCTGGTTT GTCGACCAAA scrFI ecoRII ATGCACCAGG TACGTGGTCC GACCGAAGGC CTGGCTTCCG 11 AGACATTACT TCTGTAATGA aluI AAGCTCAATG TTCGAGTTAC scri ecol	GTAGATGATG GTAGATGATG GTAGATGATG GTAGATGATG ACTGGCTCAA TGACCGAGTT TCCACAGGTG AGGTGTCCAC GTGGAGTGCCAC GTGGAGTGCACAC GTGGAGTGCACACACACACACACACACACACACACACACA	mn11 hg1A TGGAGGTGCA ACCTCCACGT TGGCAAGGAG ACCGTTCCTC aI TACACCATTC ATGTGGTAAG AGTGGAATGG TCACCTTACC mn11 CAACTGCGAG GTTGACCCTC 3A I TCCCACGTCC	ddeI aluI hg CACAGCTCAG GTGTCGAGTC TTCAAATGCA AAGTTTACGT mnlI CACCTCCCAA GTGGAGGGTT fnuHI bbV GCAGCCAGCC GCTCGGTCGC GCTCGGTCGC GCTCGGTCGC mnlI CTTGCGGCCC mnlI CTTGCGGCCC mnlI CTTGCGGCCC mnlI CTTGCGGCCC mnlI CTTGCGGCCC mnlI CTTGCGGCCC mnlI CTTGCGCCCC mnlI CTTGCGGCCC mnlI CTTGCGGCCC mnlI CTTGCGGCCC mnlI CTTGCGGCCC mnlI CTTGCGGCCCC mnlI CTTGCGCCCCC mnlI CTTGCGCCCC mnlI CTTGCGCCC mnlI CTTGCCCCC mnlI CTTGCCCCC mnlI CTTGCCCCC mnlI CTTGCCCC mnlI CTTGCCCC mnlI CTTGCCCC mnlI CTTGCCCC mnlI CTTGCCC mnlI CTTGCCCC mnlI CTTGCCC mnlI CTTGCC mnlI CTTGCC mnlI CTTGCCC mnlI CTTGCC mnlI CTTCC mnlI CTTGCC mnlI CTTCC mnlI	GACTCCTAAG CTGAGGATTC smal scr scr nci ncil hpa aI avai ACGCAACCCC TGCGTTGGGG hinclI GGGTCAACAG CCCAGTTGTC ha hae CCCAGTTGTC GAGAGCAGATG CCTCGTCTAC SAMAGTGGAC sau96 avaii	FI II III mnli GGGAGGAGCA CCCTCCTCGT fnu4HI bbv alul T6CAGCTTTC ACGTCGAAAG eIII I GCCAAGGATA CGGTTCCTAT ddeI AGAACACTCA CTTGTGGAGT CTCTGTGTAA	TTGTGGTAGA AACACCATCT GTTCAACAGC CCAGCTCGCCCCA GGACGGGGGT AAGTCAGTCT (TTCAGTCAGC (GCCCATCATG A CGGGTAGTAC 1 sau96 mn11 haelIII CATGAGGGGC A GTACTCCCGG A	CATCAGCAAG GTAGTCGTTC dde ACTTTCCGCT TGAAAGGCGA tagI TCGAGAAAAAC AGCTCTTTTG GACCTGCATG ACACCAACCA TGTGCTTAC CCGTGTTGGT GCACAACCA CCGTGTTGGT mn11	GATGATCCCG CTACTAGGGC I CAGTCAGTGA GTCAGTCACT CATCTCCAAAA STAGAGGTTT ATAACAGACT IATTGTCTGA CCTCTTACTT CGAGAATGAA mbol ddel CCATACTGAG GTATGACTC
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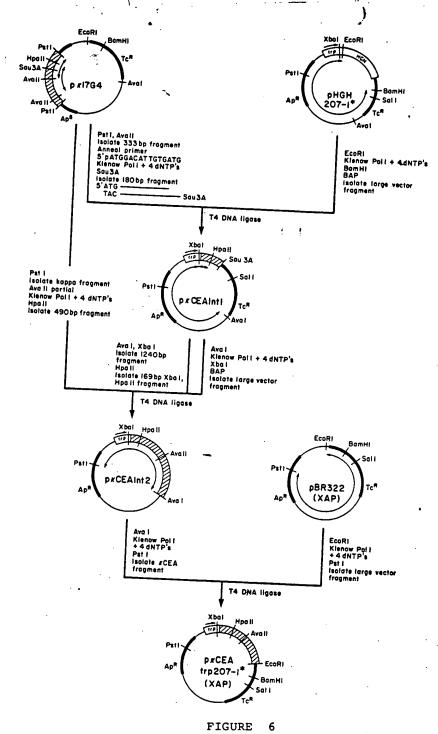
p gamma 298 cDNA insert and py 11 cDNA insert ligation containing coding sequence for heavy (gamma) anti CEA chain

val met leu val glu ser gly gly val leu met glu pro gly gly ser leu lys leu ser cys ala ala ser gly phe thr phe ser arg GUG AUG CUG GUG GAG UCU GGG GGA GUC UUA AUG GAG CCU GGA GGG UCC CUG AAA CUC UCC UGU GCA GCC UCU GGA UUC ACU UUC AGU AGA 40 50 tyr ala met ser trp val arg gln thr pro glu lys arg leu glu trp val ala thr ile ser ser gly gly ser ser his leu pro ser UAU GCC AUG UCU UGG GUU CGC CAG ACU CCG GAG AAG AGG CUG GAG UGG GCC ACC AUU AGU AGU AGU GGU AGU UCA CAC CUU CCA UCC arg gln cys glu gly arg phe thr ile ser arg asp asn ala lys asn thr leu tyr leu gln met ser ser leu arg ser glu asp thr AGA CAG UGU GAA GGG CGA UGU ACC AUC UCC AGA GAC AAU GCC AAG AAC ACC CUG UAC CUG CAA AUG AGC AGU CUG AGG UCU GAG GAC ACG 100 120
ala met tyr tyr cys ala arg pro pro leu ile ser leu val ala asp tyr ala met asp tyr trp gly gln gly thr ser val thr val
GCC AUG UAU UAC UGU GCA AGA CCC CCU CUU AUU UCG UUA GUA GCG GAC UAU GCU AUG GAC UAC UGG GGU CAA GGA ACC UCA GUC ACC GUC ser ser ala lys thr thr pro pro ser val tyr pro leu ala pro gly ser ala ala gln thr asn ser met val thr leu gly cys leu UCC UCA GCC AAA ACG ACA CCC CCA UCU GUC UAU CCA CUG GCC CCU GGA UCU GCU GCC CAA ACU AAC UCC AUG GUG ACC CUG GGA UGC CUG val lys gly tyr phe pro glu pro val thr val thr trp asn ser gly ser leu ser ser gly val his thr phe pro ala val leu gln GUC AAG GGC UAU UUC CCU GAG CCA GUG ACA GUG ACC UGG AAC UCU GGA UCC CUG UCC AGC GGU GUG CAC ACC UUC CCA GCU GUC CAG ser asp leu tyr thr leu ser ser ser val thr val pro ser ser pro arg pro ser glu thr val thr cys asn val ala his pro ala UCU GAC CUC UAC ACU CUG AGC CAC CUG AGC CAC GUC ACC GUC ACC GUC CAC CAC GCC ser ser thr lys val asp lys lys ile val pro arg asp cys gly cys lys pro cys ile cys thr val pro glu val ser ser val phe AGC AGC ACC AAG GAC AAA AUU GUG CCC AGG GAU UGU GGU UGU AAG CCU UGC AUA UGU ACA GUC CCA GAA GUA UCA UCU GUC UUC ile phe pro pro lys pro lys asp val leu thr ile thr leu thr pro lys val thr Cys val val val asp ile ser lys asp asp pro AUC DUC CCC CCA AAG CCC AAG GAU GUC CCC AUU ACU CUG ACU CCU AAG GUC ACG UGU GUU GUG GUA GAC AUC AGC AAG GAU GAU CCC ser val ser glu leu pro ile met his gln asp trp leu asn gly lys glu phe lys cys arg val asn ser ala ala phe pro ala pro UCA GUC AGU GAA CUU CCC AUC AUG CAC CAG GAC UGG CUC AAU GGC AAG GAG UUC AAA UGC AGG GUC AAC AGU GCA GCU UUC CCU GCC CCC 340

11e glu lys thr ile ser lys thr lys gly arg pro lys ala pro gln val tyr thr ile pro pro pro lys glu gln met ala lys asp
AUC GAG AAA ACC AAC CUC CAAA ACC AAA GGC AGA CCG AAG GCU CCA CAG GUG UAC ACC AUU CCA CCU CCC AAG GAG CAG AUG GCC AAG GAU 380 lys val ser leu thr cys met ile thr asp phe phe pro glu asp ile thr val glu trp gln trp asn gly gln pro ala glu asn tyr AAA GUC AGU CUG ACC UGC AUG AUA ACA GAC UUC UUC CCU GAA GAC AUU ACU GUG GAG UGG CAG UGG AAU GGG CAG CCA GCG GAG AAC UAC lys asn thr gln pro ile met asn thr asn gly ser tyr phe val tyr ser lys leu asn val gln lys ser asn trp glu ala gly asn AAG AAC ACU CAG CCC AUC AUG AAG AAC ACG AAU GGC UCU UAC UCC GUC UAC AGC AAG CUC AAU GUG CAG AAG AAC AAC UGG GAG GCA GGA AAU thr phe thr cys ser val leu his glu gly leu his asn his his thr glu lys ser leu ser his ser pro gly lys OP ACU UUC ACC UGC UCU GUG UUA CAU GAG GGC CUG CAC AAC CAC CAU ACU GAG AAG AGC CUC UCC CAC UCU CCU GGU AAA UGA UCCCAGUGUCCU

FIGURE 5

Amino acid and coding sequence for heavy (gamma-1) anti CEA chain



Construction of plasmid for direct expression of light anti CEA (kappa) chain gene

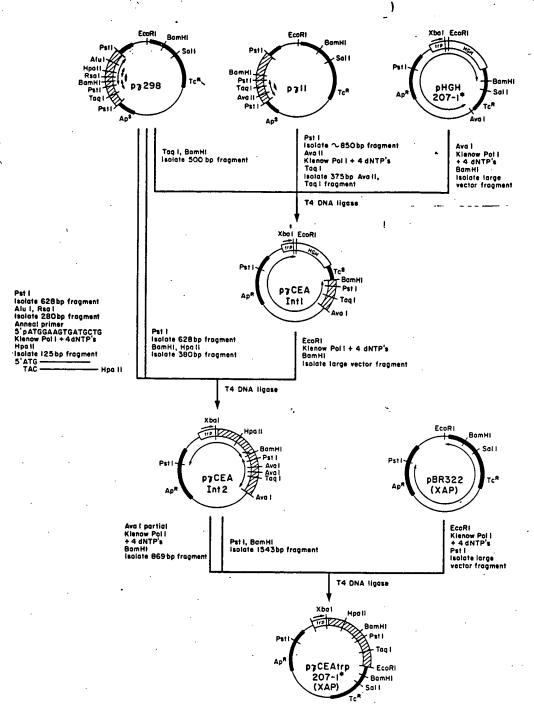


FIGURE 7

Construction of plasmid for direct expression of anti
CEA light (gamma 1) chain

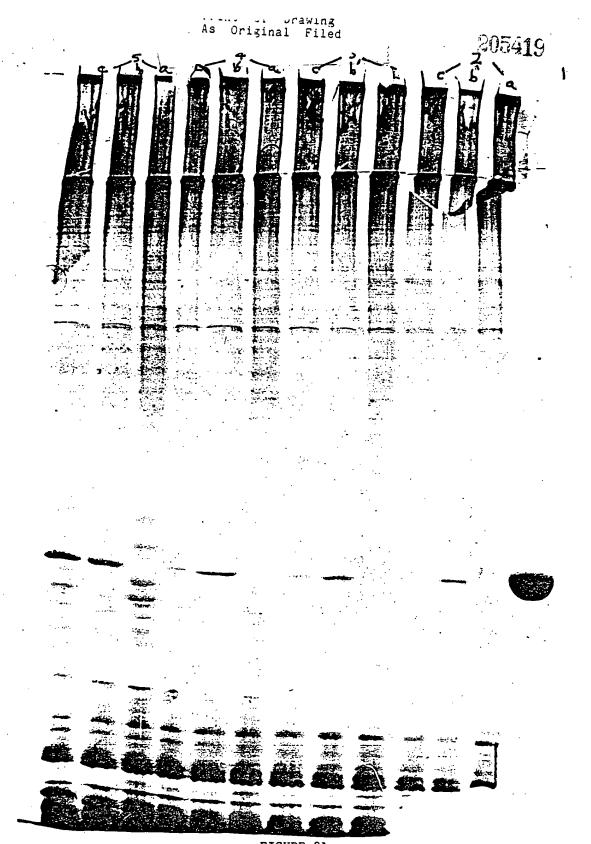


FIGURE 8A
Silver stained SDS-PAGE of extracts from E. coli transformed with pyCEAtrp207-

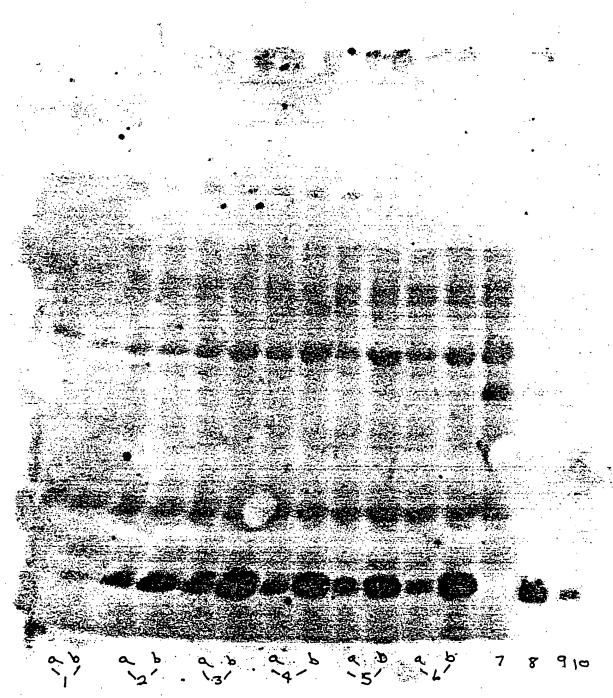


FIGURE 8B

Western blot of SDS PAGE performed on extracts of $\underline{E}.\underline{coli}$ transformed with PKCEAtrp207-1*

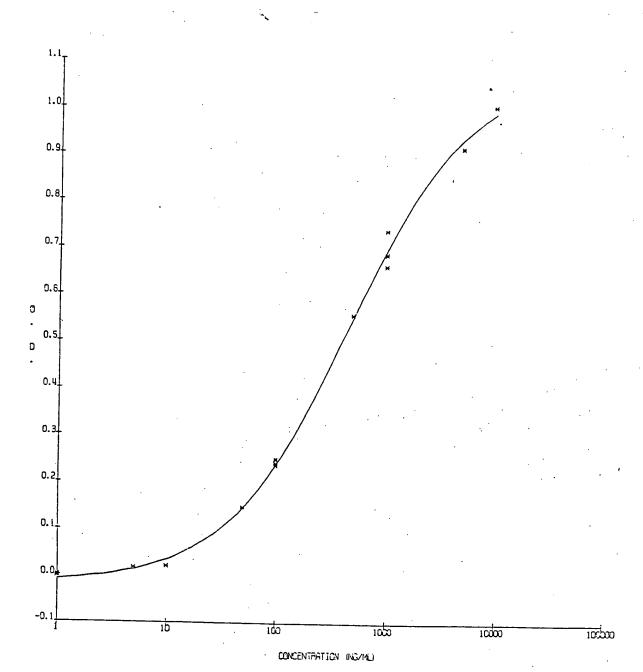


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FIGURE 8C Western blot of SDS PAGE E. coli double transformed with pkCEAtrp207-1*4 and pyCEAInt2.

1.00ug anti-CEA k cells (10ul) \$ cells (10ul) 0.10ug anti-CEA 0.30ug anti-CEA 0.05ug anti-CEA k% cells (10ul) k**%** cells (20úl) k cells (20ul) 31-3531-35 k-675 RW57-k 3000 RW57-K3000 210ng 700ng . <u>3</u>0ng 90ng 300ng

Western blot of SDS PAGE performed on extracts of E. coli transformed with plasmids containing to DNA sequences and coding heavy light and both heavy and light anti CEA chains.



in in

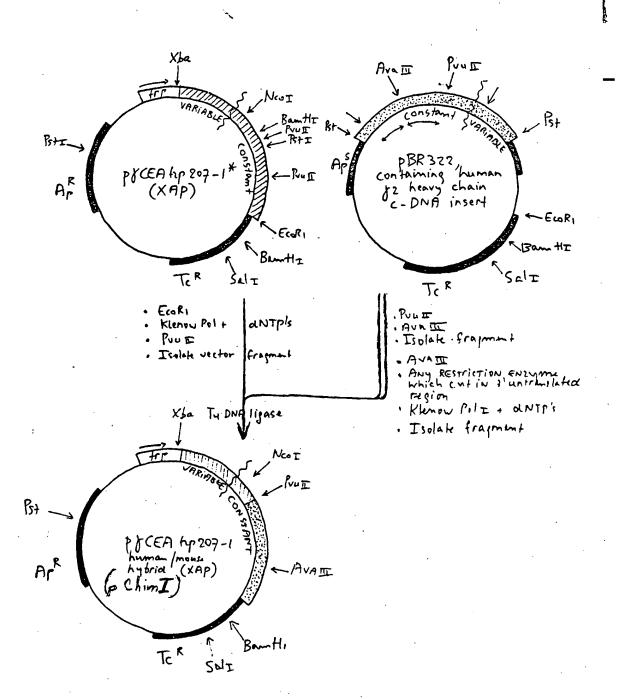
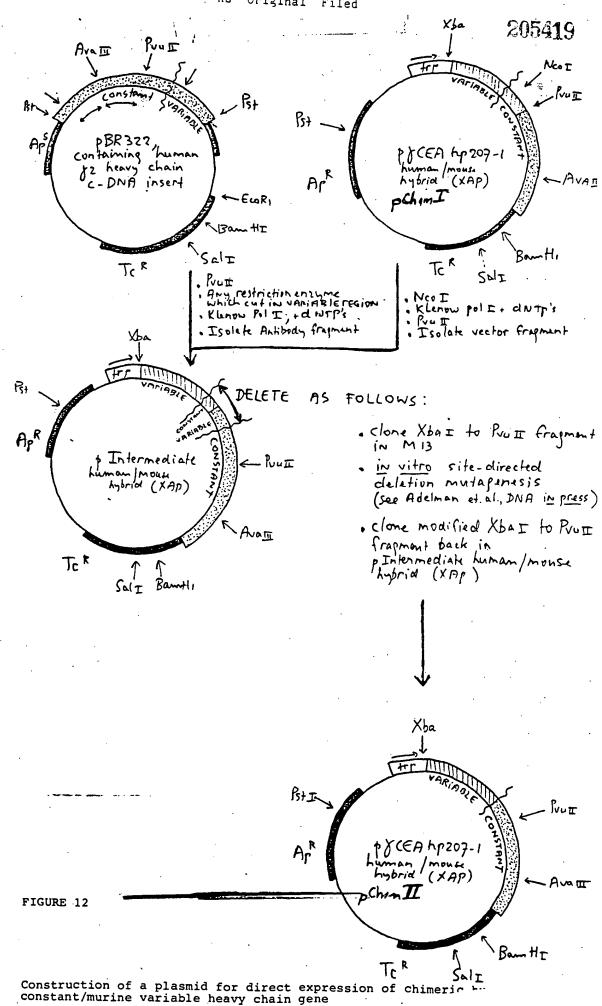


FIGURE 11

Construction of a plasmid for direct expression of chimeric human/murine heavy chain gene



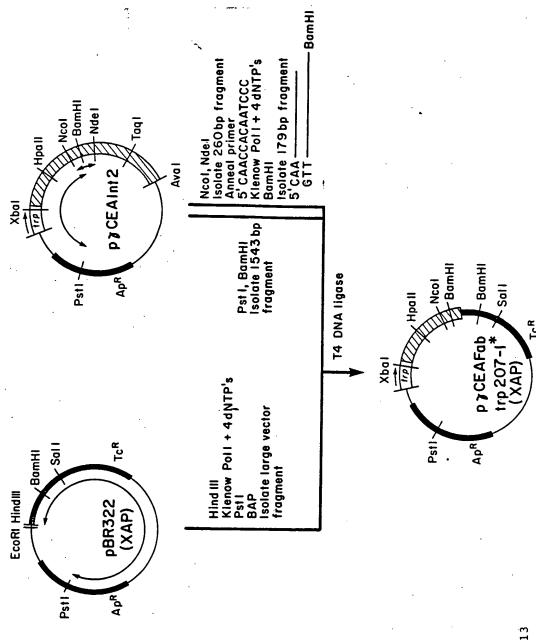


FIGURE 13

Construction of plasmid for direct expression of Fab region from heavy anti CEA chain gene

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